



No new matter has been added with this amendment.

Claims 11-31 have been cancelled without prejudice. Applicants reserve the right to file a division and/or continuation on the cancelled subject matter.

Rejection under 35 U.S.C. § 102(b)

The Examiner has rejected Claims 5, 9, and 10 under 35 U.S.C. § 102 (b) as anticipated by WO96/08582. The Examiner states that the cited reference discloses *S. epidermidis* primers. This rejection, to the extent that it applies to the claims as amended is respectfully traversed.

To anticipate a claim under 35 U.S.C. § 102 (b), the reference must contain all of the elements of the claimed limitations. WO 96/08582 contains 4 primers that consist of no more than 25 to 30 nucleotides. Claims 9 and 10 as amended claim a probe or isolated nucleotide sequence that comprises at least 40 nucleotides of the SEQ ID NO:1835. Claim 5 also has been amended to obviate the alleged rejection. Thus WO 96/08582 does not anticipate the claimed invention.

The Examiner has rejected Claims 5, 9, and 10 under 35 U.S.C. § 102 (b) as anticipated by U.S. Patent No. 5,770,375 ('375 patent). The Examiner identifies Example 2 and 3 of the '375 patent as containing *S. epidermidis* primers which correlate to SEQ ID NO:5 – SEQ ID NO:8 of the '375 patent. The Applicants have provided the Examiner Exhibits A-D describing with sequence alignments between the claimed sequence SEQ ID NO:1835 and SEQ ID NO:5 – SEQ ID NO:8 disclosed in the Patent '375. As shown in Exhibits A-D detailing the alignments, the sequence overlaps do not exceed 20 bases. Moreover, the amended claims providing the number of nucleotide bases as 40 bases in claims 9 and 10 and the number the 10 amino acids of claim 5, overcome the alleged rejection under 35 U.S.C. § 102 (b).

Withdrawal of these rejections is respectfully requested.

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Conclusion

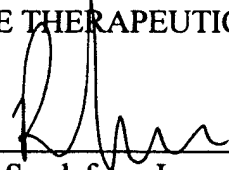
Reconsideration and withdrawal of the pending rejections are respectfully requested and a Notice of Allowance is earnestly solicited.

If the Examiner feels that a telephone conference would expedite prosecution of this application, he is invited to call the undersigned at 781-398-2300.

Any deficiency or overpayment for this reply should be charged or credited to Deposit Account No. 50-1040. One duplicate copy of this letter is enclosed.

Respectfully submitted,

GENOME THERAPEUTICS CORPORATION

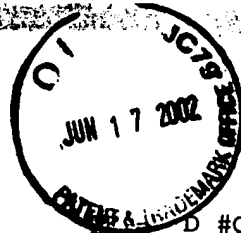
By 
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Waltham, Massachusetts 02453

Dated:

4/3/02

SEQ ID NO:5 vs SEQ ID NO:1835



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Q = CGI_26caws20d648.seq
T = SEQ
A =
D = ID NO:1835
Identical Match = 282 Similar = 282 Total # Of Gaps = 41
Identity: Alignment = 54% Query = 11% Target = 54%
Similarity: Alignment = 54% Query = 11% Target = 54%
QS = 487 QE = 974 TS = 2 TE = 434
D #Q Symbols = 2362
D #T Symbols = 519

Q 487 AAAAAGCTTGAATTTTACAAGATAACGGA-AATGTTAAGAG-GAGA-AAGCTGATTGATT
A A ACTT T TTAC GA AA GGA AAT TA GAG AGA AAG A T ATT
T 2 AGATACTT----TGTTACTTGAAAAAGGAGAATAATATGAGTAAGACAAGAGCAGTTATT

Q 544 CACTTTAACTATGATAGAACATTATCAGTTATTG---CTGAAATAAAATCGAA--AAGC-
C C TA T TGAT A ATTA CA TAT G CT A ATA AT GAA AAGC
T 58 CCCGGTAGTTTTGATCCA--ATTA-CA--TATGGTCACTTAGATATCATTGAAAGAAGCG

Q 598 CCATCTGTACCTCAATTACCGCAACGTGATCTTGTTCAACAAGTTAAAGATTATCAAAAA
CC C G C T AT A C A GT TTGT A AA AAA A TA AAA
T 113 CCGACCG--CTTTGATGAAATCCATGT----TTGTGTACTAA--AAAATAGTAGTAAA--

Q 658 TATGGTGCTAATGCTATTTCAATATTAAGTATGAA--AAATACTTTGGCGGTAGTTTTG
GGTG AA G TTT A T C GA GAA A AC TTG G AG T
T 163 ---GGTG-GAACG---TTTGACT-----CAGAAGAACGCATGACGTTGATTGAAGAGT--

Q 716 AACGATTAAATCAGTTATCAAAGATAACATCGTTACCAGTTTTATGTAAAGAT--TTTAT
CG TTAAA CA TT C AA AT ACA A CA TTT ATG A G T TT AT
T 209 --CGGTTAAA-CATTTGCCTAATAT-ACAAGTGCATCATTTTAATGGATTGCTTGTGAT

Q 774 TATTGATAAAATTCAAATAGATGTTGCAAAACGAGCTGGTGCATCTATTATTTTA---TT
T TTG A TCAA TA G TGCAAA GA C ATTATT A TT
T 265 TTTTGTGA----TCAAGTA---GGTGCAAA--GA-----CAATTATTCGAGGTTT

Q 831 AATA---GTAAAT-ATTTTAAGTGATGACCAATTAAAAGAATTGTATTCATATGCAACAA
AA A GTAA T A TTT A T ATGA C A GA T TA T TATG AACAA
T 306 AAGAGCTGTAAGTGACTTTGAAT-ATGAAC-----TACGACT--TACTTCTATG-AACAA

Q 887 ACCATAATTTAGAAGCTCTAGTAGAAGTTCATACAAT-TAGAGAAGCTTGA-ACGTGCACA
A AA TTA A TAGTA A TT A ACAAT TA A A TGA A GTGCA A
T 357 A----AAGTTAAA-----TAGTA-ATATTGAAACAATGTACATGA--TGACAAGTGCAAA

Q 945 CCA---AATTAACCCTAAAATTATTGGTGTAA
C A A TTA T AA TAT TGTTAA
T 405 CTATTCATTTATAAGTTCAAGTAT---TGTTAA

EXHIBIT A

SEQ ID NO:6 vs SEQ ID NO:1835



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RANK 1 Score = 322.00 P_Score = -1.0e+00

Q = CGI_26cbws24d66a.seq

QF = D #Q Symbols = 8654

T = SEQ

TF = D #T Symbols = 519

A =

D = ID NO:1835

Identical Match = 234 Similar = 234 Total # Of Gaps = 30

Identity: Alignment = 55% Query = 2% Target = 45%

Similarity: Alignment = 55% Query = 2% Target = 45%

QS = 2974 QE = 3380 TS = 62 TE = 429

```
Q   2974 GTATTTTGGAGTTCCTCATATAAATGATCTTTTTCATA--ATTGTAATATTCTAACACTG
      GTA TTT GA  TCC  TA A ATG TC  TT  ATA  ATTG AA A   A C C
T     62 GTAGTTTTGA--TCCAATTACATATGGTCACTTAGATATCATTGAAAGA----AGCGC-C

Q   3032 GAGTGTTTTTAGATACTTTGCTATGATTTTTTACTAAAAGTTTTTGGAGTTGTCCTAAAG
      GA  G TTT A   A T   C ATG TT T TACTAAAA           A T GT  TAAAG
T     115 GACCGCTTTGATGAAAT---CCATGTTTGTGTACTAAAA-----AATAGTAGTAAAG

Q   3092 TGGGAGTGTAGTAGAAAATATAGCTGTTAAGAGGGGCTTGTATACCAGTTG-TTGAAAGG
      GT GAA  T T  CT   AAGA  GC TG   AC  GTTG TTGAA  G
T     164 -----GTGGAACGTTTGACTCAGAAGA-ACGCATG---AC--GTTGATTGAA--G

Q   3151 AGTAATTTGGGC-TTTG-CTTTTATA-GTTTTTATATTTTAAATATCTTCTGTTTTAGAA
      AGT  TT   C TTTG CT  TATA   T  AT  TTTTAAT   T  TG TT
T     206 AGTCGGTTAAACATTTGCCTAATATACAAGTGCATCATTTTAATGGAT--TGCTT-----

Q   3208 GTTAATTT---AGAGAAAGTA-ATGTAATAAACTA--CAAGTTGTGAGA-ATGAAAAT
      GTT ATTT   GA  AAGTA  TG AA  A AA TA  C AG T T AGA  TG AA T
T     259 GTTGATTTTTGTGATCAAGTAGGTGCAAGACAATTATTTCGAGGTTTAAGAGCTGTAAGT

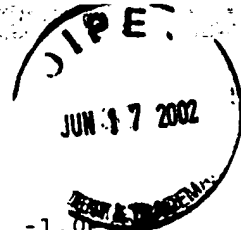
Q   3261 GAATAGTAATGAAGAAATAACGA-TGCGTTGCTTGGTCATGGATGTTACCTCATAATAT
      GA T   AAT A GAA T ACGA T   TT   TG  CA   A GTT A   ATA TA
T     319 GACTTTGAAT-ATGAACT-ACGACTTACTTCTATGAACA-AAAAGTTAA----ATAGTAA

Q   3320 TATTGTGAGGTTATTATACACTATTATTTTAAATGAAATATATTAATTT-TAAAT--AAG
      TATTG  A   A T TAC  AT AT   AA TG AA  TATT ATTT TAA T  AAG
T     372 TATTGAAA---CAATGTAC---ATGATGACAAGTGCAAACTATTTCATTTATAAGTTCAAG

Q   3377 CATT
      ATT
T     426 TATT
```

EXHIBIT B

SEQ ID NO:7 vs SEQ ID NO:1835



RANK 1 Score = 345.00 P_Score = -1.00

Q = CGI_26ccws22157d.seq

QF = D #Q Symbols = 5024

T = SEQ

TF = D #T Symbols = 519

A =

D = ID NO:1835

Identical Match = 156 Similar = 156 Total # Of Gaps = 17

Identity: Alignment = 56% Query = 3% Target = 30%

Similarity: Alignment = 56% Query = 3% Target = 30%

QS = 3068 QE = 3318 TS = 225 TE = 474

Q 3068 TGATATAGAA---CCCTTTTGTATGTCTTATGATAAATTAATAGACTTTTGTAAAAAAC
T ATATA AA C TTTT ATG GAT TT T GA TTTTGT A AA
T 225 TAATATACAAGTGCATCATTTTAAATG-----GATTGCTT-GTTGATTTTGTGATCAAG

Q 3124 AAGCT--ATAGACAAAGTTGTTGTTGCAGGTGATATTATGAGTTATCA-TCACGAAGAAT
AG T A AGACAA TT TT AGGT TTA GAG T T A T AC GAAT
T 278 TAGGTGCAAAGACAA-----TTATTCGAGGT----TTAAGAGCTGTAAGTGACTTTGAAT

Q 3181 ATG----ACATTTTACATCAAAGGA-AACGATTTAAACAAGCTAATATTCAAGTAATAT-
ATG AC TTAC TC A G A AA A TTAAA A TAATATT AA AAT T
T 329 ATGAACTACGACTTACTTCTATGAACAAAAAGTTAAATA--GTAATATTGAAACAATGTA

Q 3235 CAT-----TAAGAGCAAATCATT-ATTT-TAACCCCGCAAAACACATAATAAACAAGGG
CAT AAG GCAAA ATT ATTT TAA G AA T TAAA AAG
T 387 CATGATGACAAGTGCAAATTCATTTATAA-----GTTCAAGTATTGTTAAAGAAGTA

Q 3288 GAACCATATAAAG----TATTTACCAGTTTTTATA
G CATAT AAG ATTT CA TTTT TA
T 442 GCTGCATATCAAGCGGACATTT--CACCTTTTGTA

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EXHIBIT C

SEQ ID NO:8 vs SEQ ID NO:1835



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RANK 1 Score = 288.00 P_Score = -1.0e+00

Q = CGI_26cdws332f0b.seq

QF = D #Q Symbols = 3287

T = SEQ

TF = D #T Symbols = 519

A =

D = ID NO:1835

Identical Match = 233 Similar = 233 Total # Of Gaps = 29

Identity: Alignment = 55% Query = 7% Target = 44%

Similarity: Alignment = 55% Query = 7% Target = 44%

QS = 1617 QE = 2014 TS = 134 TE = 519

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Q   1617 ATGTCAGGCTATCGAAATTATCAGTATTTAA-GTGA----CTGGCAAAGAGAAC-CAT
      ATGT  G  TA C AAA  AT AGTA T AA GTGA      TG C  A  AGAAC CAT
T   134 ATGTTTGTGTA-CTAAAAAAT-AGTAGTAAAGGTGGAACGTTTGACTCAGAAGAACGCAT

Q   1671 -TCTTTGGTGTTCATTTGTCGTGGTAATTTTTGC----TATAGGTGGCGTACCTCCTTT
      C TTG  TTG A  GTCG  AA TTTGC  TATA      GT C TC TTT
T   192 GACGTTG--ATTG-AAGAGTCGGTTAAACATTTGCCTAATATA---CAAGTGCATCATTT

Q   1726 TAGTGGCTTTCCGGGTAAAGTCTTAATATTCCA--AGGGGCTATTACAAATGGTAATTAT
      TA TGG TT C  G T A  T TT  T  TC A  AGG GC A  ACAA  T ATT
T   246 TAATGGATTGCTTGTGA--TTTTTGTGATCAAGTAGGTGCAAAGACAA----TTATTGC

Q   1784 ATTGGTTTAGCACTTATGATTGTGACAAGTTTAATTGCTATGTA-TAGTCTTTTAGAGT
      A GGTTTA A  T T A  GTGAC  TTT A  TATG A TA  C  TTA
T   300 A--GGTTTAAGAGCTGTAA--GTGAC---TTTGA---ATATGA ACTA--CGACTTACTTC

Q   1843 GATGTTTATAATGTATTTTGGTGATGCTGACGGAGAACAA-GTACAATTTAGACCA---C
      ATG  A AA GT  T GT AT  TGA      AACAA GTAC AT  GAC A  C
T   348 TATGAACAAAAAGTTAAATAGTAATATTGA-----AACAAATGTAC-ATGATGACAAGTGC

Q   1899 TACCTATTTATCGTAAAGGTTTACTTAGTGTTTTAGTTGTAGTGGTATTAGCGA-TGGGT
      A CTATT AT  TA A GTT A  TA TGTT  AG  GTAG  G A TA C A  GG
T   402 AAAC TATTCAT-TTATAAGTTCAAGTATTGTTAAAGAAGTAGCTGCA-TATCAAGCGGAC

Q   1958 ATTGCAGCCCCTGTTGT----TCTGAAAGTAACAGAGGATGCAACA--AATCTTAATATG
      ATT CA  CCT TTGT  CT A  A AGAG AT  AA A  AA  TTAAT T
T   460 ATTTCA---CCTTTTGTACCACCTCATGTCGAAAGAGCATTAAAAAAGAAATTTAATGTT

Q   2012 AAA
      AA
T   517 TAA
  
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EXHIBIT D



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CLAIMS

5 1. (Amended) An isolated nucleic acid comprising a nucleotide sequence
encoding an *S. epidermidis* polypeptide ~~selected from the group consisting of~~ SEQ ID
NO: 3773 ~~SEQ ID NO: 7544~~ 5607.

10 5. (Amended) An isolated nucleic acid comprising a nucleotide sequence
encoding an *S. epidermidis* polypeptide or a fragment of at least ten amino acid residues
thereof, said nucleic acid ~~selected from the group consisting of~~ SEQ ID NO: 1835 ~~SEQ~~
~~ID NO: 3772~~.

15 9. (Amended) A probe comprising a nucleotide sequence consisting of at least
fortyeight contiguous nucleotides of a nucleotide sequence ~~selected from the group~~
~~consisting of~~ SEQ ID NO: 4 ~~SEQ ID NO: 3772~~ 1835.

20 10. (Amended) An isolated nucleic acid comprising a nucleotide sequence of at
least ~~eight~~ forty nucleotides in length, wherein the sequence is hybridizable to a nucleic
acid having a nucleotide sequence ~~selected from the group consisting of~~ SEQ ID NO: 4 ~~SEQ~~
~~ID NO: 3772~~ 1835.

Clean Version Claims

CLAIMS



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- 5 1. (Amended) An isolated nucleic acid comprising a nucleotide sequence
encoding an *S. epidermidis* polypeptide of SEQ ID NO:5607.
5. (Amended) An isolated nucleic acid comprising a nucleotide sequence
encoding an *S. epidermidis* polypeptide or a fragment of at least ten amino acid residues ,
10 said nucleic acid of SEQ ID NO:1835.
9. (Amended) A probe comprising a nucleotide sequence consisting of at least
forty contiguous nucleotides of a nucleotide sequence of SEQ ID NO:1835.
- 15 10. (Amended) An isolated nucleic acid comprising a nucleotide sequence of at
least forty nucleotides in length, wherein the sequence is hybridizable to a nucleic acid
having a nucleotide sequence of SEQ ID NO: 1835.